

Patented Dec 22, 1993

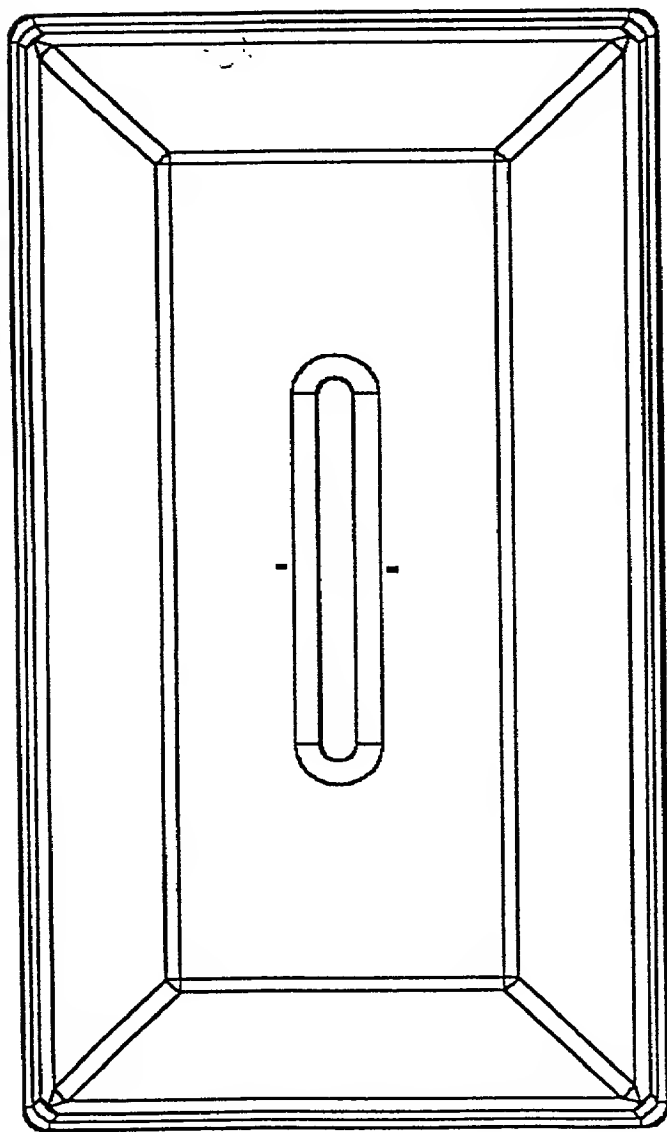


Figure 1A

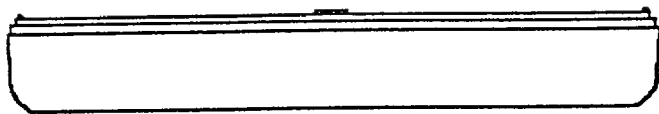


Figure 1C



Figure 1B

Figure 3A

Nucleotide sequence of *Cryptosporidium parvum* protein disulfide isomerase cDNA

5 001 atgatcggaa ttagaagctt ggtttcagca gcatttttag gtttttcttg tcttccaag
061 gtagtcttgg gtggagatga agctcacttc atttcagaac acattacttc cttaacttcc
121 tccaacttcg aagacttcat taagagcaag gaacacgtaa ttgttacttt ctttgcccca
10 181 tgggtcggcc attgtactgc tttagagcca gaattcaagg caacatgcgc tgaatctca
241 aagctctctc cccagtaca ctgtggcagt gttgatgcaa ctgaaaatat ggagcttgca
301 caacaatatg gtgtgagcgg ataccgaac atcaaatctt tcagtgggat tgacagtgtt
361 cagaactatt caggagcaag aagcaaggat gcattcatca agtatattaa gaagtggacc
421 ggaccagcag tccaagtgc tgaatcagaa gaagctatca agacaatctt cgcttcttct
15 481 tcttcagcct ttgttggaag attcacctct aaggactcag ctgagtatgc tgtcttcgag
541 aaggttgcta gtgtcacccg cgagcacaac tatgctttca ttgctttctt ccaagaaggt
601 gaacaaaagc tcgaggattt acacaaggac gaggagccag ttctctctcc aatgccaaaag
661 actgttgaa agttggaggc caagatatcc ataatgaatg taccattgtt ctctgcaatt
721 agtgctgaga actactccct ctatatgtca agagaagggt atactgcctgg ttctgtggtta
20 782 ctaacgagga cttcgccaa gtgcttcaa acattagaaa ggttgcagct gattacagag
842 aaaagtatgc ctttggtttc _cttgatact gagcaatttg gttcccatgc tactcaacat
901 ctcttaattg agaaattccc aggtttggtt atccaaagtg tcaatgttcc atcaattaga
961 tacatgtatg gtccagctaa attcgactct gttgagccat taaaggaatt tatgaagcaa
1021 gtttctgaag gcaagcacga actcagcatt aagtctgagc caatcccagc tgagcaatct
1081 ggtccagtca ctgttgttgt tggtaagacc ttcgaagaaa ttgttttcag aagtgacaag
25 1141 gatgttctt ttgaaatcta tgccaatgg tgtggacact gtaagaacct cgagccaatc
1201 tacaaccaac tcggcgaa ga gtacaaggac aacgacaagg ttgtgattgc aaagatcaat
1261 ggaccacaaa acgatatccc atatgaaggt ttcagtccaa ggccttccc aactatcttg
1321 ttcgtcaagg ccggaactag aacccaatt cttatgatg gaaagagaac tgttgaggcc
1381 ttcaagggaat tcatcagtga acatttcttc tccctcaag aaaaggaatc tcgtgacgaa
30 1441 ctctaa

Figure 3B

Deduced Amino Acid Sequence of *C. parvum* Protein Disulfide Isomerase

5 MIGIRSLVSA AFLGFSCLSKVVLGGDEAHFISEHITSLTSSNFEDFIKSKEHVIVTFFAP
61 WCGHCTALEPEFKATCAEISKLSPPVHCGSVDATENMELAQQYGVSGYPTIKFFSGIDSV
121 QNYSGARSKDAFIKYIKKLTGPAVQVAESEEAIKTIFASSSAFVGRFTSKDSAEYAVFE
181 KVASGHRHNYAFIAFFQEGEQKLEVLHKDEEPVSLPMPKTVEELEAKISIMNVPLFSAI
241 SAENYSLYMSREGYTAWFCGTNEDFAKYASNIRKVAADYREKYAFVFLDTEQFGSHATQH
10 301 LLIEKFPGLVIQSVNVPSIRYMYGPAKFDSVEPLKEFMKQVSEGHHELSEKSEPIP AEQS
361 GPVTVVVGKTFEEIVFRSDKDVLLIYAQWCGHCKNLEPIYNQLGEEYKDNDKVVIAKIN
421 GPQNDIPYEGFSPRAFPPTILFVKAGTRTPIPYDGGKRTVEAFKEFISEHSSFPQEKESRDEL